

OIPE

RAW SEQUENCE LISTING

DATE: 07/23/2001

PATENT APPLICATION: US/09/782,587

TIME: 13:17:25

Input Set : A:\31001lus.app

Output Set: N:\CRF3\07232001\I782587.raw

3 <110> APPLICANT: PEDERSEN, ANDERS H.
 4 ANDERSON, KIM V.
 5 BORNAES, CLAUS
 7 <120> TITLE OF INVENTION: FACTOR VII OR VIIA-LIKE MOLECULES
 9 <130> FILE REFERENCE: 31-001100US
 11 <140> CURRENT APPLICATION NUMBER: 09/782,587
 12 <141> CURRENT FILING DATE: 2001-02-12
 14 <150> PRIOR APPLICATION NUMBER: PA 2000 00218
 15 <151> PRIOR FILING DATE: 2000-02-11
 17 <150> PRIOR APPLICATION NUMBER: 60/184,036
 18 <151> PRIOR FILING DATE: 2000-02-22
 20 <150> PRIOR APPLICATION NUMBER: 60/241,916
 21 <151> PRIOR FILING DATE: 2000-10-18
 23 <160> NUMBER OF SEQ ID NOS: 19
 25 <170> SOFTWARE: PatentIn Ver. 2.1
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 28 <211> LENGTH: 406
 29 <212> TYPE: PRT
 30 <213> ORGANISM: Homo sapiens
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 34 <222> LOCATION: (6)..(7)
 35 <223> OTHER INFORMATION: Gamma carboxyglutamic acid or glutamic acid
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 59 <222> LOCATION: (35)
 60 <223> OTHER INFORMATION: Gamma carboxyglutamic acid or glutamic acid
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 64 1 5 10 15
 W--> 66 Cys Lys Xaa Xaa Gln Cys Ser Phe Xaa Xaa Ala Arg Xaa Ile Phe Lys

Does Not Comply
Corrected Diskette Needed

see item #9 on
error summary
sheet.

All Xaa's need
numeric identifiers
<220> - <223> and
explanation of what
Xaa is equal to.

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67          20          25          30
W--> 69 Asp Ala Xaa Arg Thr Lys Leu Phe Trp Ile Ser Tyr Ser Asp Gly Asp
70          35          40          45
72 Gln Cys Ala Ser Ser Pro Cys Gln Asn Gly Gly Ser Cys Lys Asp Gln
73          50          55          60
75 Leu Gln Ser Tyr Ile Cys Phe Cys Leu Pro Ala Phe Glu Gly Arg Asn
76 65          70          75          80
78 Cys Glu Thr His Lys Asp Asp Gln Leu Ile Cys Val Asn Glu Asn Gly
79          85          90          95
81 Gly Cys Glu Gln Tyr Cys Ser Asp His Thr Gly Thr Lys Arg Ser Cys
82          100          105          110
84 Arg Cys His Glu Gly Tyr Ser Leu Leu Ala Asp Gly Val Ser Cys Thr
85          115          120          125
87 Pro Thr Val Glu Tyr Pro Cys Gly Lys Ile Pro Ile Leu Glu Lys Arg
88          130          135          140
90 Asn Ala Ser Lys Pro Gln Gly Arg Ile Val Gly Gly Lys Val Cys Pro
91 145          150          155          160
93 Lys Gly Glu Cys Pro Trp Gln Val Leu Leu Leu Val Asn Gly Ala Gln
94          165          170          175
96 Leu Cys Gly Gly Thr Leu Ile Asn Thr Ile Trp Val Val Ser Ala Ala
97          180          185          190
99 His Cys Phe Asp Lys Ile Lys Asn Trp Arg Asn Leu Ile Ala Val Leu
100          195          200          205
102 Gly Glu His Asp Leu Ser Glu His Asp Gly Asp Glu Gln Ser Arg Arg
103          210          215          220
105 Val Ala Gln Val Ile Ile Pro Ser Thr Tyr Val Pro Gly Thr Thr Asn
106 225          230          235          240
108 His Asp Ile Ala Leu Leu Arg Leu His Gln Pro Val Val Leu Thr Asp
109          245          250          255
111 His Val Val Pro Leu Cys Leu Pro Glu Arg Thr Phe Ser Glu Arg Thr
112          260          265          270
114 Leu Ala Phe Val Arg Phe Ser Leu Val Ser Gly Trp Gly Gln Leu Leu
115          275          280          285
117 Asp Arg Gly Ala Thr Ala Leu Glu Leu Met Val Leu Asn Val Pro Arg
118          290          295          300
120 Leu Met Thr Gln Asp Cys Leu Gln Gln Ser Arg Lys Val Gly Asp Ser
121 305          310          315          320
123 Pro Asn Ile Thr Glu Tyr Met Phe Cys Ala Gly Tyr Ser Asp Gly Ser
124          325          330          335
126 Lys Asp Ser Cys Lys Gly Asp Ser Gly Gly Pro His Ala Thr His Tyr
127          340          345          350
129 Arg Gly Thr Trp Tyr Leu Thr Gly Ile Val Ser Trp Gly Gln Gly Cys
130          355          360          365
132 Ala Thr Val Gly His Phe Gly Val Tyr Thr Arg Val Ser Gln Tyr Ile
133          370          375          380
135 Glu Trp Leu Gln Lys Leu Met Arg Ser Glu Pro Arg Pro Gly Val Leu
136 385          390          395          400
138 Leu Arg Ala Pro Phe Pro
139          405

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142 <210> SEQ ID NO: 2
143 <211> LENGTH: 1338
144 <212> TYPE: DNA
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148 <221> NAME/KEY: CDS
149 <222> LOCATION: (115)..(1332)
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154 gccgtcttcg tcaccagga ggaagcccat ggcgtcctgc atcgccggcg ccgg gcc 117
155 Ala
156 1
158 aat gcc ttt ctg gaa gag ctc cgc cct ggc tcc ctg gaa cgc gaa tgc 165
159 Asn Ala Phe Leu Glu Glu Leu Arg Pro Gly Ser Leu Glu Arg Glu Cys
160 5 10 15
162 aaa gag gaa cag tgc agc ttt gag gaa gcc cgg gag att ttc aaa gac 213
163 Lys Glu Glu Gln Cys Ser Phe Glu Glu Ala Arg Glu Ile Phe Lys Asp
164 20 25 30
166 gct gag cgg acc aaa ctg ttt tgg att agc tat agc gat ggc gat cag 261
167 Ala Glu Arg Thr Lys Leu Phe Trp Ile Ser Tyr Ser Asp Gly Asp Gln
168 35 40 45
170 tgc gcc tcc agc cct tgc cag aac ggg ggc tcc tgc aaa gac cag ctg 309
171 Cys Ala Ser Ser Pro Cys Gln Asn Gly Gly Ser Cys Lys Asp Gln Leu
172 50 55 60 65
174 cag agc tat atc tgc ttc tgc ctg cct gcc ttt gag ggg cgc aat tgc 357
175 Gln Ser Tyr Ile Cys Phe Cys Leu Pro Ala Phe Glu Gly Arg Asn Cys
176 70 75 80
178 gaa acc cat aag gat gac cag ctg att tgc gtc aac gaa aac ggg ggc 405
179 Glu Thr His Lys Asp Asp Gln Leu Ile Cys Val Asn Glu Asn Gly Gly
180 85 90 95
182 tgc gag cag tac tgc agc gat cac acg ggc acg aag cgg agc tgc cgc 453
183 Cys Glu Gln Tyr Cys Ser Asp His Thr Gly Thr Lys Arg Ser Cys Arg
184 100 105 110
186 tgc cac gaa ggc tat agc ctc ctg gct gac ggg gtg tcc tgc acg ccc 501
187 Cys His Glu Gly Tyr Ser Leu Leu Ala Asp Gly Val Ser Cys Thr Pro
188 115 120 125
190 acg gtg gaa tac cct tgc ggg aag att ccc att cta gaa aag cgg aac 549
191 Thr Val Glu Tyr Pro Cys Gly Lys Ile Pro Ile Leu Glu Lys Arg Asn
192 130 135 140 145
194 gct agc aaa ccc cag ggc cgg atc gtc ggc ggg aag gtc tgc cct aag 597
195 Ala Ser Lys Pro Gln Gly Arg Ile Val Gly Gly Lys Val Cys Pro Lys
196 150 155 160
198 ggg gag tgc ccc tgg cag gtc ctg ctc ctg gtc aac ggg gcc cag ctg 645
199 Gly Glu Cys Pro Trp Gln Val Leu Leu Leu Val Asn Gly Ala Gln Leu
200 165 170 175
202 tgc ggc ggg acc ctc atc aat acc att tgg gtc gtg tcc gcc gct cac 693
203 Cys Gly Gly Thr Leu Ile Asn Thr Ile Trp Val Val Ser Ala Ala His
204 180 185 190
206 tgc ttc gat aag att aag aat tgg cgg aac ctc atc gct gtg ctc ggc 741

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207 Cys Phe Asp Lys Ile Lys Asn Trp Arg Asn Leu Ile Ala Val Leu Gly
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210 gaa cac gat ctg tcc gag cat gac ggg gac gaa cag tcc cgc cgg gtg 789
211 Glu His Asp Leu Ser Glu His Asp Gly Asp Glu Gln Ser Arg Arg Val
212 210      215      220      225
214 gct cag gtc atc att ccc tcc acc tat gtg cct ggc acg acc aat cac 837
215 Ala Gln Val Ile Ile Pro Ser Thr Tyr Val Pro Gly Thr Thr Asn His
216      230      235      240
218 gat atc gct ctg ctc cgc ctc cac cag ccc gtc gtg ctc acc gat cac 885
219 Asp Ile Ala Leu Leu Arg Leu His Gln Pro Val Val Leu Thr Asp His
220      245      250      255
222 gtc gtg cct ctg tgc ctg cct gag cgg acc ttt agc gaa cgc acg ctg 933
223 Val Val Pro Leu Cys Leu Pro Glu Arg Thr Phe Ser Glu Arg Thr Leu
224      260      265      270
226 gct ttc gtc cgc ttt agc ctc gtg tcc ggc tgg ggc cag ctg ctc gac 981
227 Ala Phe Val Arg Phe Ser Leu Val Ser Gly Trp Gly Gln Leu Leu Asp
228      275      280      285
230 cgg ggc gct acc gct ctc gag ctg atg gtg ctc aac gtc ccc cgg ctg 1029
231 Arg Gly Ala Thr Ala Leu Glu Leu Met Val Leu Asn Val Pro Arg Leu
232 290      295      300      305
234 atg acc cag gac tgc ctg cag cag tcc cgc aaa gtg ggg gac tcc ccc 1077
235 Met Thr Gln Asp Cys Leu Gln Gln Ser Arg Lys Val Gly Asp Ser Pro
236      310      315      320
238 aat atc acg gag tat atg ttt tgc gct ggc tat agc gat ggc tcc aag 1125
239 Asn Ile Thr Glu Tyr Met Phe Cys Ala Gly Tyr Ser Asp Gly Ser Lys
240      325      330      335
242 gat agc tgc aag ggg gac tcc ggc ggg ccc cat gcc acg cac tat cgc 1173
243 Asp Ser Cys Lys Gly Asp Ser Gly Gly Pro His Ala Thr His Tyr Arg
244      340      345      350
246 ggg acc tgg tac ctc acc ggg atc gtc agc tgg ggc cag ggc tgc gcc 1221
247 Gly Thr Trp Tyr Leu Thr Gly Ile Val Ser Trp Gly Gln Gly Cys Ala
248      355      360      365
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251 Thr Val Gly His Phe Gly Val Tyr Thr Arg Val Ser Gln Tyr Ile Glu
252 370      375      380      385
254 tgg ctg cag aag ctc atg cgg agc gaa ccc cgg ccc ggg gtg ctc ctg 1317
255 Trp Leu Gln Lys Leu Met Arg Ser Glu Pro Arg Pro Gly Val Leu Leu
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259 Arg Ala Pro Phe Pro
260      405
263 <210> SEQ ID NO: 3
264 <211> LENGTH: 406
265 <212> TYPE: PRT
266 <213> ORGANISM: Homo sapiens
268 <400> SEQUENCE: 3
269 Ala Asn Ala Phe Leu Glu Glu Leu Arg Pro Gly Ser Leu Glu Arg Glu
270 1      5      10      15
272 Cys Lys Glu Glu Gln Cys Ser Phe Glu Glu Ala Arg Glu Ile Phe Lys

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```

273          20          25          30
275 Asp Ala Glu Arg Thr Lys Leu Phe Trp Ile Ser Tyr Ser Asp Gly Asp
276          35          40          45
278 Gln Cys Ala Ser Ser Pro Cys Gln Asn Gly Gly Ser Cys Lys Asp Gln
279          50          55          60
281 Leu Gln Ser Tyr Ile Cys Phe Cys Leu Pro Ala Phe Glu Gly Arg Asn
282          65          70          75          80
284 Cys Glu Thr His Lys Asp Asp Gln Leu Ile Cys Val Asn Glu Asn Gly
285          85          90          95
287 Gly Cys Glu Gln Tyr Cys Ser Asp His Thr Gly Thr Lys Arg Ser Cys
288          100          105          110
290 Arg Cys His Glu Gly Tyr Ser Leu Leu Ala Asp Gly Val Ser Cys Thr
291          115          120          125
293 Pro Thr Val Glu Tyr Pro Cys Gly Lys Ile Pro Ile Leu Glu Lys Arg
294          130          135          140
296 Asn Ala Ser Lys Pro Gln Gly Arg Ile Val Gly Gly Lys Val Cys Pro
297          145          150          155          160
299 Lys Gly Glu Cys Pro Trp Gln Val Leu Leu Val Asn Gly Ala Gln
300          165          170          175
302 Leu Cys Gly Gly Thr Leu Ile Asn Thr Ile Trp Val Val Ser Ala Ala
303          180          185          190
305 His Cys Phe Asp Lys Ile Lys Asn Trp Arg Asn Leu Ile Ala Val Leu
306          195          200          205
308 Gly Glu His Asp Leu Ser Glu His Asp Gly Asp Glu Gln Ser Arg Arg
309          210          215          220
311 Val Ala Gln Val Ile Ile Pro Ser Thr Tyr Val Pro Gly Thr Thr Asn
312          225          230          235          240
314 His Asp Ile Ala Leu Leu Arg Leu His Gln Pro Val Val Leu Thr Asp
315          245          250          255
317 His Val Val Pro Leu Cys Leu Pro Glu Arg Thr Phe Ser Glu Arg Thr
318          260          265          270
320 Leu Ala Phe Val Arg Phe Ser Leu Val Ser Gly Trp Gly Gln Leu Leu
321          275          280          285
323 Asp Arg Gly Ala Thr Ala Leu Glu Leu Met Val Leu Asn Val Pro Arg
324          290          295          300
326 Leu Met Thr Gln Asp Cys Leu Gln Gln Ser Arg Lys Val Gly Asp Ser
327          305          310          315          320
329 Pro Asn Ile Thr Glu Tyr Met Phe Cys Ala Gly Tyr Ser Asp Gly Ser
330          325          330          335
332 Lys Asp Ser Cys Lys Gly Asp Ser Gly Gly Pro His Ala Thr His Tyr
333          340          345          350
335 Arg Gly Thr Trp Tyr Leu Thr Gly Ile Val Ser Trp Gly Gln Gly Cys
336          355          360          365
338 Ala Thr Val Gly His Phe Gly Val Tyr Thr Arg Val Ser Gln Tyr Ile
339          370          375          380
341 Glu Trp Leu Gln Lys Leu Met Arg Ser Glu Pro Arg Pro Gly Val Leu
342          385          390          395          400
344 Leu Arg Ala Pro Phe Pro
345          405

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VERIFICATION SUMMARY

PATENT APPLICATION: US/09/782,587

DATE: 07/23/2001

TIME: 13:17:27

Input Set : A:\31001lus.app

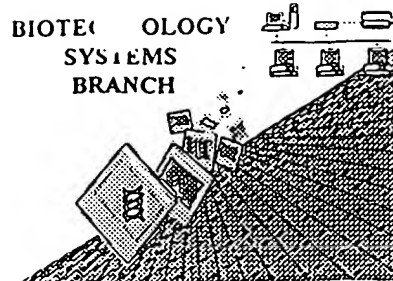
Output Set: N:\CRF3\07232001\I782587.raw

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L:66 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1

L:69 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1

RAW SEQUENCE LISTING ERROR REPORT



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/782,587

Source: OIPE

Date Processed by STIC: 7/23/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>